

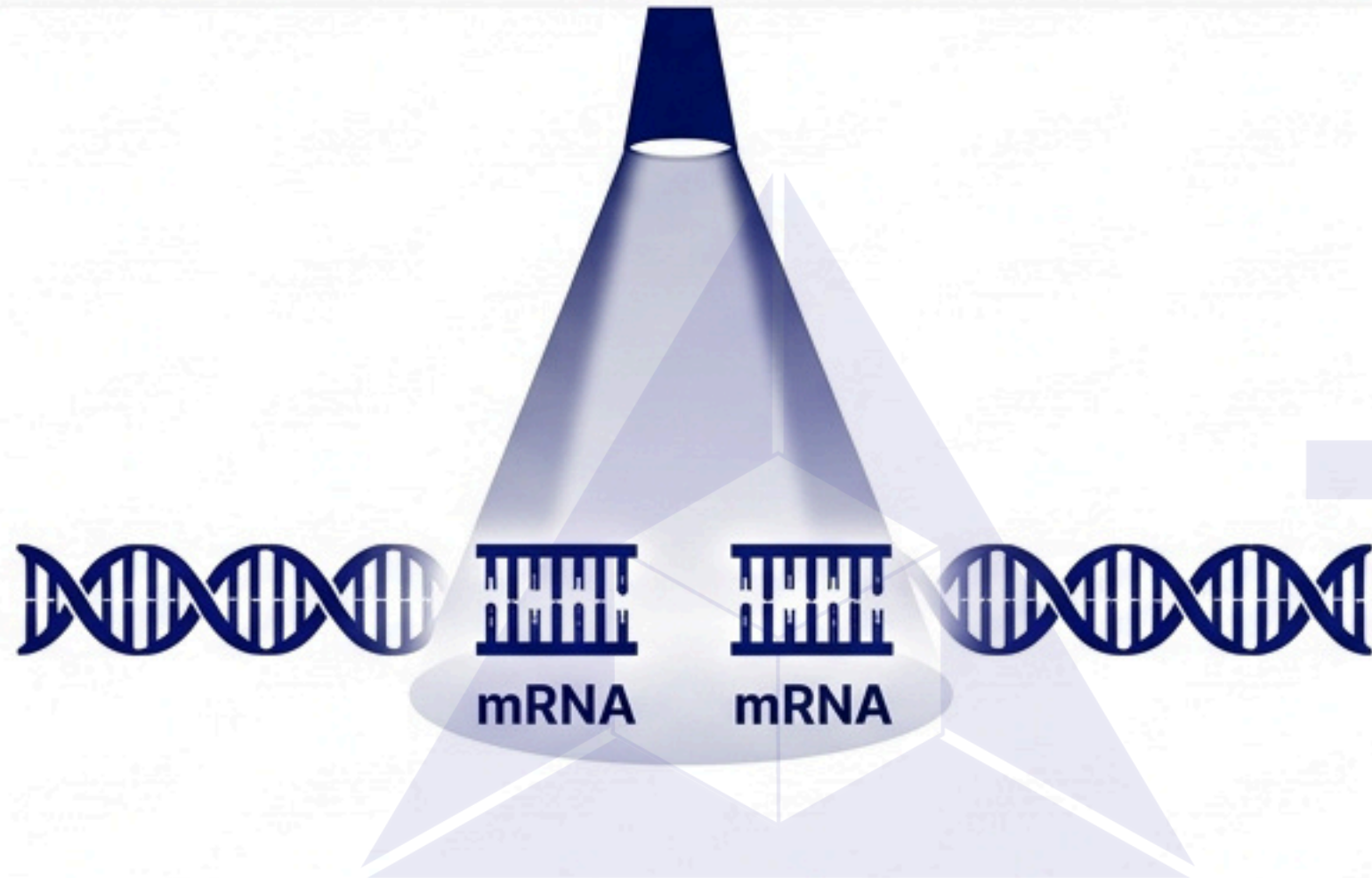
How HGP Sequenced the Genome



Methodologies and Workflows of a 3-Billion Base Pair Project



Two Strategic Approaches



Expressed Sequence Tags (ESTs)

Focuses exclusively on identifying all the genes that are expressed as RNA (the coding regions).



Sequence Annotation

The blind approach of sequencing the entire genome (coding + non-coding sequences), and later assigning functions to different regions.



**You've Learned the Theory.
Let's Test Them Now.**

$$E=mc^2$$



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Key Highlights

- » Free Study Material, Videos & Infographics
- » Push Your Limits with Level-Based Challenges
- » Climb the Leaderboard Among Fellow Aspirants
- » Practice Unlimited MCQs for NEET & JEE
- » Get Clear Explanations, Not Just Marks
- » Track Your Performance Smarter



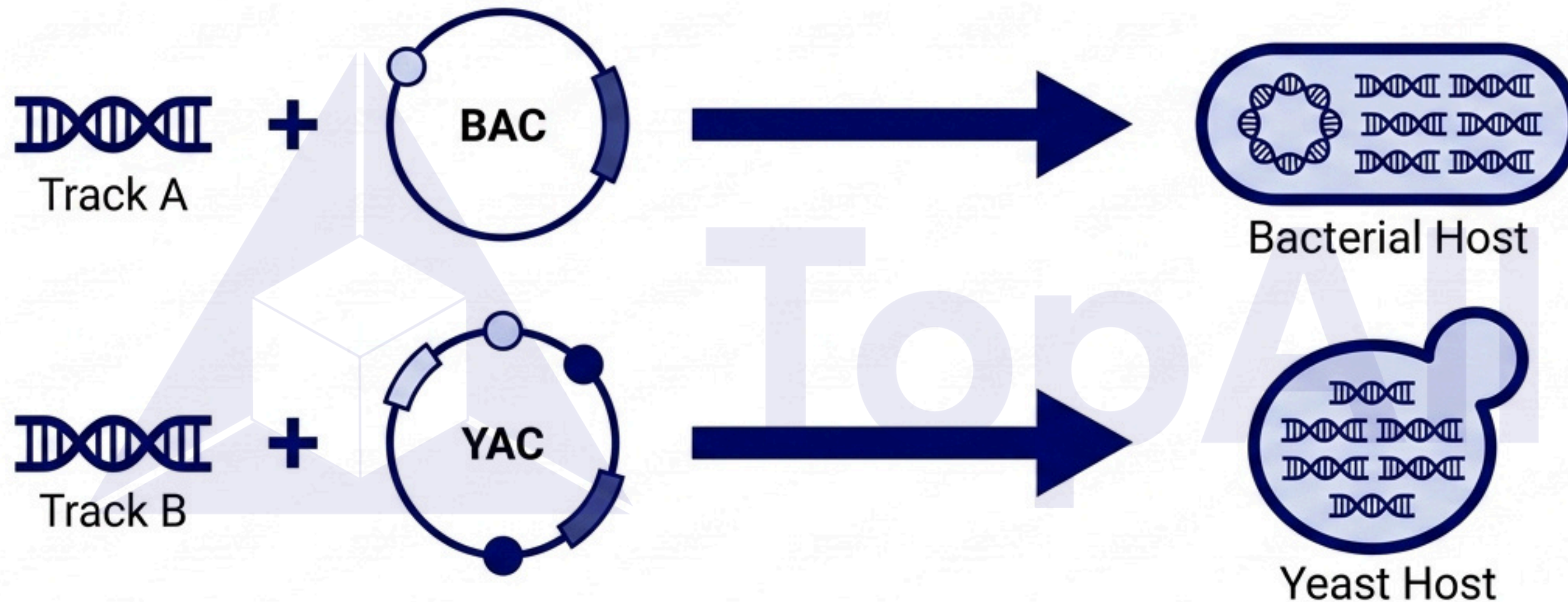
Step 1: Isolation & Fragmentation



Why fragment the DNA?

There are strict technical limitations in sequencing very long polymers. DNA must be converted into random, smaller fragments to be read accurately.

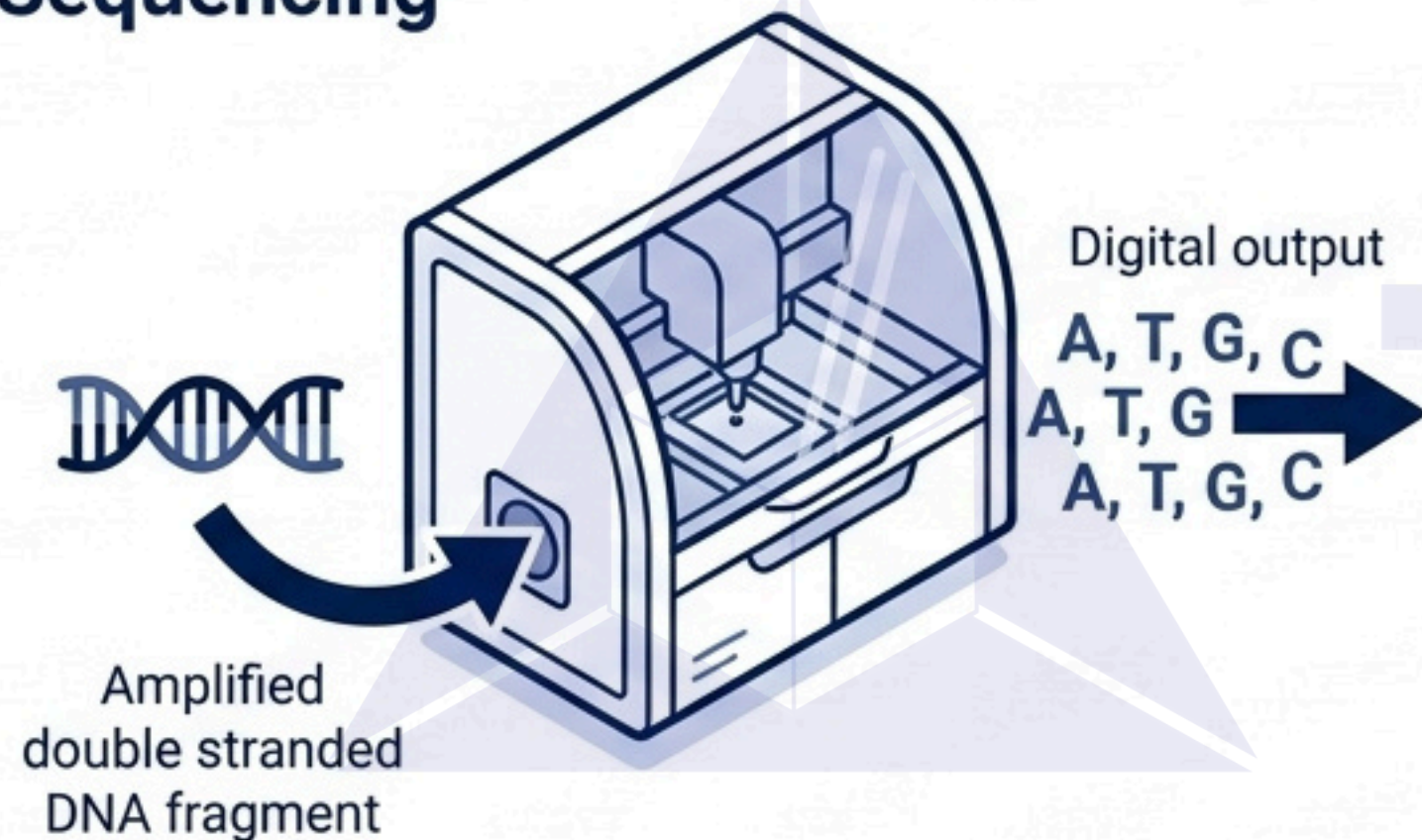
Step 2: Amplification via Vectors



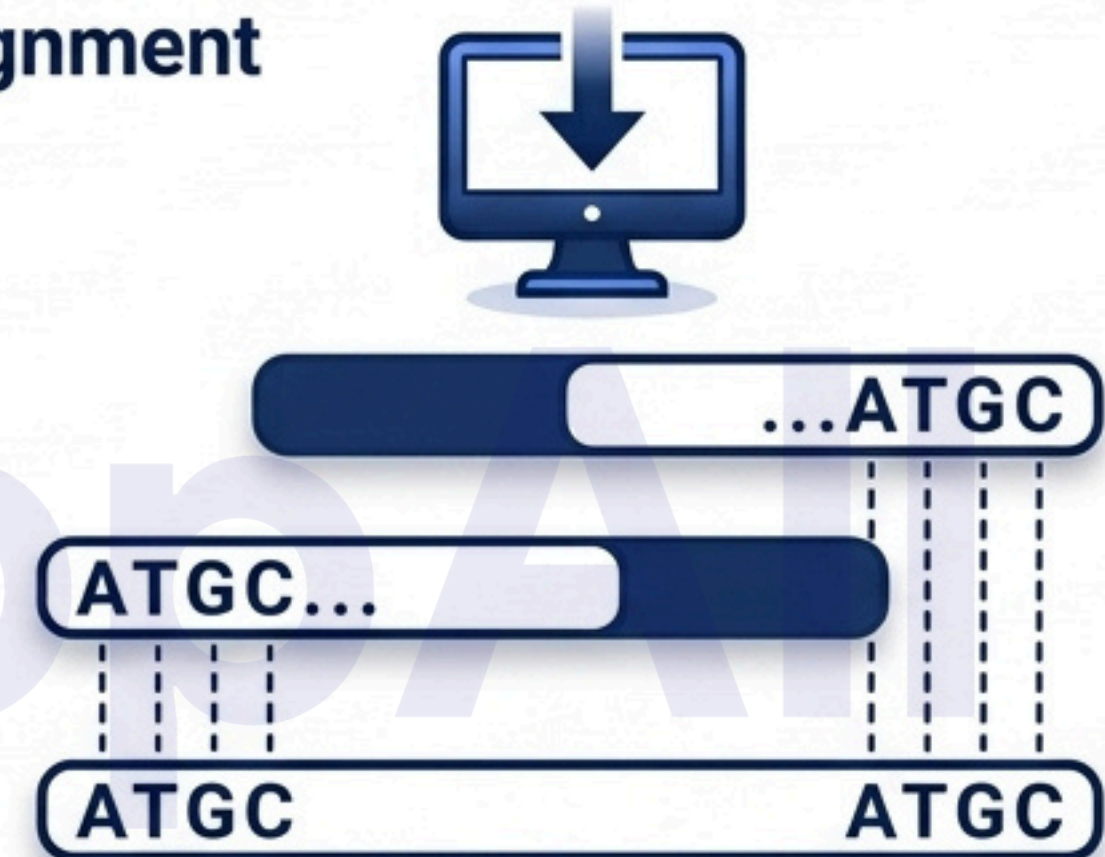
Cloning into these specialized hosts results in the **amplification** of each DNA fragment, creating enough identical copies so they can subsequently be sequenced with ease.

Step 3 & 4: Automated Sequencing & Alignment

Sequencing

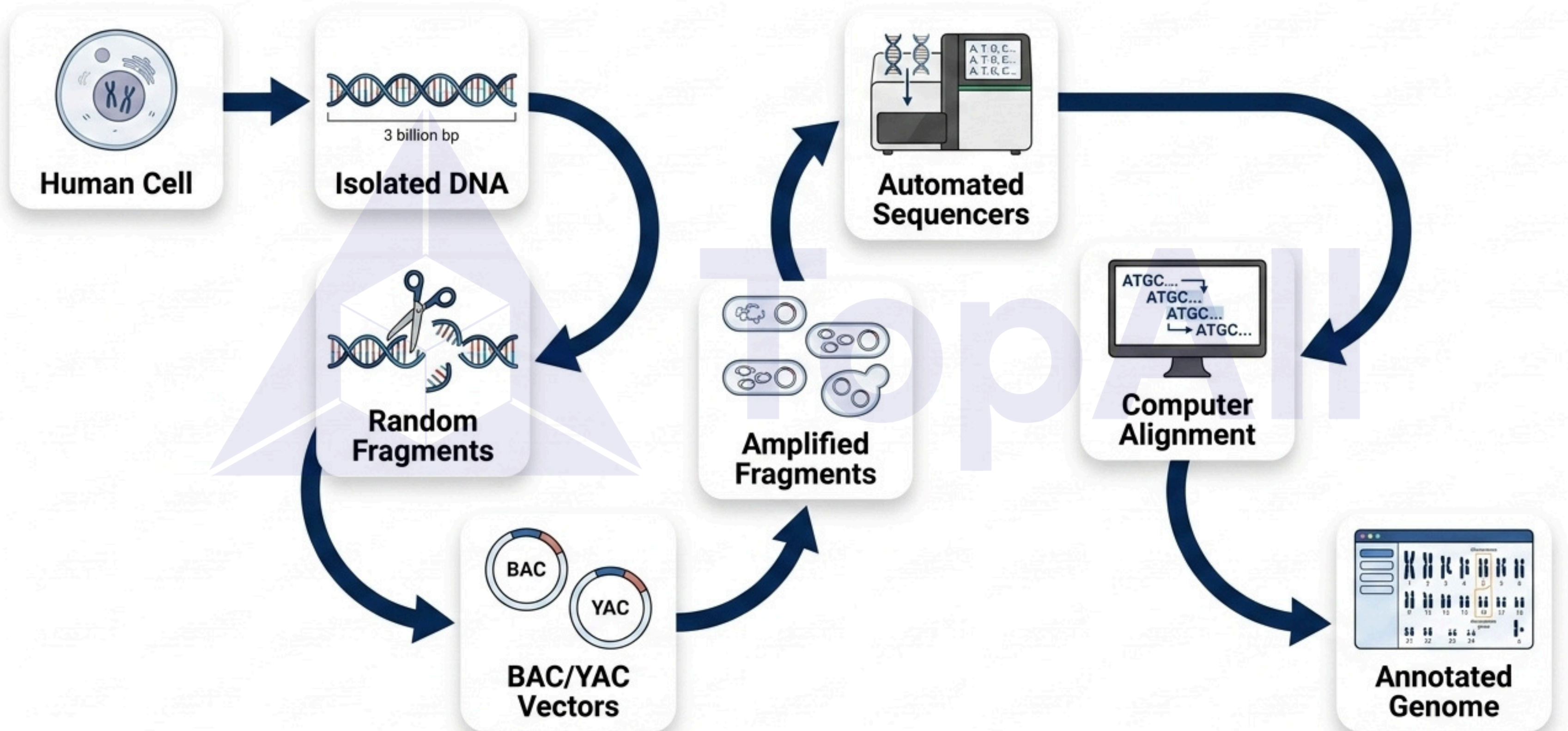


Alignment



Alignment of these sequences was humanly not possible. It required specialized computer-based programs to arrange fragments based on overlapping regions, giving rise to the field of Bioinformatics.

The HGP Workflow: Master Synthesis





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